SEQUENCE LISTING

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SOMERVILLE, Chris

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921
<141> 1999-03-04

<150> 08/597,313
<151> 1996-02-06

<150> PCT/US97/02187
<151> 1997-02-06

<160> 15

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Lesquerella fendleri

<220>
<221> primer_bind
<222> (83)
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attctggtgt taacagttca gtttatcctc gggtggcctt tgtatctagc ctttaatgta 180
tcaggtagac cttatgatgg tttcgcttca catttcttcc ctcatgcacc tatctttaag 240
gaccgtgaac gtctccagat atacatctca gatgctggta ttctagctgt ctgttatggt 300
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ttacctcact atgattcaac cgagtgggaa tggattagag gagctttggt tacggtagac 480
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cac 543

<210> 2
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atcatgatgt taactgtcca gttcgtcctc ggatggccct tgtacttagc cttcaacgtt 180

tctggcagac cctacaatgg tttcgcttcc catttcttcc ccaatgctcc tatctacaac 240
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ctttaccgtt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagttccg 360
cttctgatag ttaacttttt cctcgtcttg atcacttact tacaacacac tcaccctgcg 420
ttgcctcact atgattcatc agagtgggat tggcttagag gagctttagc tactgtagac 480
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<211> 1855
<212> DNA
<213> Lesquerella fendleri

<220>
<221> gene
<222> (1)..(1855)
<223> genomic clone encoding pLesq-HYD

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agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcatcgtta 300
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<210> 4
<211> 384
<212> PRT
<213> Lesquerella fendleri

<400> 4

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 1               5                  10                  15

Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
            20                  25                  30

Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
        35                  40                  45

Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
    50                  55                  60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65                  70                  75                  80

Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
                85                  90                  95

Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
            100                 105                 110

Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
        115                 120                 125

Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
    130                 135                 140

His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
145                 150                 155                 160

Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
                165                 170                 175

Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
            180                 185                 190

Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
        195                 200                 205

Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu
    210                 215                 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
225                 230                 235                 240

Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
                245                 250                 255

Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
            260                 265                 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
        275                 280                 285

Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile
```

a' cont

```
    290                 295                 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305                 310                 315                 320

Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
                325                 330                 335

Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
            340                 345                 350

Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
        355                 360                 365

Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
    370                 375                 380
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<210> 5
<211> 387
<212> PRT
<213> Ricinus communis

<400> 5

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  1               5                  10                  15

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
             20                  25                  30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
         35                  40                  45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
     50                  55                  60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
 65                  70                  75                  80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
                 85                  90                  95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
            100                 105                 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
        115                 120                 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
    130                 135                 140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
145                 150                 155                 160
```

```
Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
                165                 170                 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
            180                 185                 190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
        195                 200                 205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
    210                 215                 220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
225                 230                 235                 240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
                245                 250                 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
            260                 265                 270

Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
        275                 280                 285

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
    290                 295                 300

Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
305                 310                 315                 320

Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
                325                 330                 335

Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
            340                 345                 350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
        355                 360                 365

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
    370                 375                 380

Asn Lys Tyr
385
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a' cont.

<210> 6
<211> 383
<212> PRT
<213> Arabidopsis thaliana

<400> 6

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  1               5                  10                  15

Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
             20                  25                  30
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Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65 70 75 80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
85 90 95

Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145 150 155 160

Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
165 170 175

Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
195 200 205

His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
210 215 220

Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
225 230 235 240

Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
245 250 255

Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
290 295 300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
305 310 315 320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
325 330 335

a1 cont

Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
340 345 350

Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
355 360 365

Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
370 375 380

<210> 7
<211> 384
<212> PRT
<213> Brassica napus

<220>
<221> PEPTIDE
<222> (1)..(384)
<223> encodes for hydroxylane enzyme for Brassica napus

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Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro
65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg
145 150 155 160

Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly
165 170 175

Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr
180 185 190

Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys
195 200 205

His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
210 215 220

Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu
225 230 235 240

Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg
245 250 255

Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
290 295 300

Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu
305 310 315 320

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
325 330 335

Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val
340 345 350

Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
355 360 365

Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu Xaa
370 375 380

a' cont.

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<211> 309
<212> PRT
<213> Glycine max

<400> 8
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Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Gln Pro
20 25 30

Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu
35 40 45

Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val

```
     50                  55                  60

Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr
 65                  70                  75                  80

Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser
                 85                  90                  95

Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu
            100                 105                 110

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
        115                 120                 125

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
    130                 135                 140

Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr
145                 150                 155                 160

Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val
                165                 170                 175

Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro
            180                 185                 190

Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val
        195                 200                 205

His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr
    210                 215                 220

Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr
225                 230                 235                 240

Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His
                245                 250                 255

Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr
            260                 265                 270

Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val
        275                 280                 285

Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn
    290                 295                 300

Lys Tyr Leu Arg Val
305
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a' cont

<210> 9
<211> 302
<212> PRT
<213> Glycine max

<400> 9

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Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe Cys Leu Tyr Tyr
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Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro Leu Ser Phe Arg
            20                  25                  30

Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val
        35                  40                  45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly
    50                  55                  60

Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr
65                  70                  75                  80

Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu
                85                  90                  95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg
            100                 105                 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu
        115                 120                 125

Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr
    130                 135                 140

Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu
145                 150                 155                 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala
                165                 170                 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe
            180                 185                 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp
        195                 200                 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
    210                 215                 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
225                 230                 235                 240

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr
                245                 250                 255

Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala
            260                 265                 270

Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly
        275                 280                 285

Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val
    290                 295                 300
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a' cont.

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<213> Zea mays

<220>
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<222> (372)
<223> Desaturase

<400> 10

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Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val
             20                  25                  30

Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro
         35                  40                  45

His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His
     50                  55                  60

Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile
 65                  70                  75                  80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp
                 85                  90                  95

Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val
            100                 105                 110

Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys
        115                 120                 125

Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp
    130                 135                 140

Glu Val Phe Val Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro
145                 150                 155                 160

Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln
                165                 170                 175

Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg
            180                 185                 190

Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr
        195                 200                 205

Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val
    210                 215                 220

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp
225                 230                 235                 240
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a' cont.

```
Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp
                245                 250                 255

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His
            260                 265                 270

Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met
        275                 280                 285

Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
    290                 295                 300

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
305                 310                 315                 320

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His
                325                 330                 335

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu
            340                 345                 350

Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn
        355                 360                 365

Lys Lys Phe Xaa
    370
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<210> 11
<211> 224
<212> PRT
<213> Ricinus communis

<400> 11

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Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln
  1               5                  10                  15

Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val
             20                  25                  30

Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr
         35                  40                  45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser
     50                  55                  60

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
 65                  70                  75                  80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe
                 85                  90                  95

Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro
            100                 105                 110

Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser
        115                 120                 125
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Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile
    130                 135                 140

Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu
145                 150                 155                 160

Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His
                165                 170                 175

Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly
            180                 185                 190

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
        195                 200                 205

His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro
    210                 215                 220
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<210> 12
<211> 20
<212> DNA
<213> Ricinus communis

<400> 12
gctcttttgt gcgctcattc 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homologous regions of Ricinus communis deduced by hydroxylase sequence and Arabidopsis thaliana deduced desaturase sequence for use as oligonucleotide primer

<400> 13
cggtaccaga aaacgccttg 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)..(20)
<223> n is any nucleotide in mixed oligonucleotide primer

<220>
<223> Description of Artificial Sequence: homologous regions of Ricinus communis deduced by hydroxylase sequence and Arabidopsis thaliana deduced desaturase sequence for u

<400> 14
taywsncaym gnmgncayca 20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homologous regions of Ricinus communis deduced by hydroxylase sequence and Arabidopsis thaliana deduced desaturase sequence for u

a' cont

<220>
<221> primer_bind
<222> (1)..(21)
<223> n is any nucleotide in mixed oligonucleotide primer

<400> 15
rtgrtgngcn acrtgngtrt c 21